AMENDMENTS

Amendments to the Claims:

Please cancel claims 3, 5-8, 10, 43 and 56-59 without prejudice or disclaimer, please amend claims 1, 4, 42 and 44, and please enter new claims 60-73 as set forth in the complete listing of the claims that follows. This complete listing of the claims replaces previous claim listings.

1 (currently amended). A method for identifying a subject at risk of breast cancer, which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a human subject, wherein the one or more polymorphic variations are detected in a region between about chromosome position 117912256 and about chromosome position 117995524, wherein each chromosome position is according to Build 31 of the GenBank database human genome sequence, ~~nucleotide sequence selected from the group consisting of:~~

~~(a) a nucleotide sequence in SEQ ID NO: 1;~~

~~(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1;~~

~~(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1;~~

~~(d) a fragment of a nucleotide sequence of (a), (b), or (c);~~

whereby the presence of the polymorphic variation is indicative of the subject being at risk of breast cancer.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (cancelled).

4 (currently amended). The method of claim 1, wherein the one or more polymorphic variations are detected within a region between about chromosome position 117925391 and about chromosome position 117945870 ~~spanning positions 13191 to 33670 in SEQ ID NO: 1~~.

5-8 (cancelled).

9 (original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

10-41 (cancelled).

42 (currently amended). A method for detecting or preventing breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a human subject, wherein the polymorphic variation is detected in a region between about chromosome position 117912256 and about chromosome position 117995524, wherein each chromosome position is according to Build 31 of the GenBank database human genome sequence, ~~nucleotide sequence selected from the group consisting of:~~

~~(a) a nucleotide sequence in SEQ ID NO: 1;~~

~~(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1;~~

~~(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1;~~

~~(d) a fragment of a nucleotide sequence of (a), (b), or (c);~~ and

administering a breast cancer preventative or detection procedure to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

43 (cancelled).

44 (currently amended). The method of claim 42 ~~claim 43~~, wherein the one or more polymorphic variations are in a region between about chromosome position 117925391 and about chromosome position 117945870 ~~spanning positions 13191 to 33670 in SEQ ID NO: 1~~.

45 (original). The method of claim 42, wherein the breast cancer detection procedure is selected from the group consisting of a mammography, an early mammography program, a frequent mammography program, a biopsy procedure, a breast biopsy and biopsy from another tissue, a breast ultrasound and optionally ultrasound analysis of another tissue, breast magnetic resonance imaging (MRI) and optionally MRI analysis of another tissue, electrical impedance (T-scan) analysis of breast and optionally of another tissue, ductal lavage, nuclear medicine analysis (e.g., scintimammography), BRCA1 and/or BRCA2 sequence analysis results, thermal imaging of the breast and optionally of another tissue, and a combination of the foregoing.

46 (withdrawn). The method of claim 42, wherein the breast cancer preventative procedure is selected from the group consisting of one or more selective hormone receptor modulators, one or more compositions that prevent production of hormones, one or more hormonal treatments, one or more biologic response modifiers, surgery, and drugs that delay or halt metastasis.

47 (withdrawn). The method of claim 46, wherein the selective hormone receptor modulator is selected from the group consisting of tamoxifen, reloxifene, and toremifene; the composition that prevents production of hormones is an aramotase inhibitor selected from the group consisting of exemestane, letrozole, anastrozol, groserelin, and megestrol; the hormonal treatment is selected from the group consisting of goserelin acetate and fulvestrant; the biologic response modifier is an antibody that specifically binds herceptin/HER2; the surgery is selected from the group consisting of lumpectomy and mastectomy; and the drug that delays or halts metastasis is pamidronate disodium.

48-59 (cancelled).

60 (new). The method of claim 4, wherein a polymorphic variation is detected at chromosome position 117925391.

61 (new). The method of claim 4, wherein a polymorphic variation is detected at chromosome position 117929437.

62 (new). The method of claim 4, wherein a polymorphic variation is detected at chromosome position 117930672.

63 (new). The method of claim 4, wherein a polymorphic variation is detected at chromosome position 117945745.

64 (new). The method of claim 4, wherein a polymorphic variation is detected at chromosome position 117945870.

65 (new). The method of claim 1, wherein a polymorphic variation is detected in a nucleotide sequence of SEQ ID NO: 1.

66 (new). The method of claim 1, wherein a polymorphic variation is detected at position 18828 of SEQ ID NO: 1.

67 (new). The method of claim 44, wherein a polymorphic variation is detected at chromosome position 117925391.

68 (new). The method of claim 44, wherein a polymorphic variation is detected at chromosome position 117929437.

69 (new). The method of claim 44, wherein a polymorphic variation is detected at chromosome position 117930672.

70 (new). The method of claim 44, wherein a polymorphic variation is detected at chromosome position 117945745.

71 (new). The method of claim 44, wherein a polymorphic variation is detected at chromosome position 117945870.

72 (new). The method of claim 42, wherein a polymorphic variation is detected in a nucleotide sequence of SEQ ID NO: 1.

73 (new). The method of claim 42, wherein a polymorphic variation is detected at position 18828 of SEQ ID NO: 1.